

1/85

FIG 1 (I)

FIG 1 (II)

FIG 1 (III)

FIG 1 (IV)

FIG 1 (V)

FIG 1

2/85

003760" 05442460

FIGURE 1 (I)

TCAGTAACA	CAGAGACTGG	GGATCGATC	ATG	GGG	CTT	TGT	AAG	TGC	CCC	50
			Met	Gly	Leu	Cys	Lys	Cys	Pro	
			1				5			
AAG AGA	AAG GTG	ACC AAC	CTG	TTC	GAA	CAT	CGG	GTC	AAC	95
Lys Arg	Lys Val	Thr Asn	Leu	Phe	Glu	His	Arg	Val	Asn	
			10	15			20			
GTC TGC	GAG CAC	TGC CTG	GTA	GCC	AAT	CAC	GCC	AAG	TGC	140
Val Cys	Glu His	Cys Leu	Val	Ala	Asn	His	Ala	Lys	Cys	
			25	30						
CAG TCC	TAC CTG	CAA TGG	CTC	CAA	GAT	AGC	GAC	TAC	AAC	185
Gln Ser	Tyr Leu	Gln Trp	Leu	Gln	Asp	Ser	Asp	Tyr	Asn	
			40	45						
TGC CGC	CTG TGC	AAC ATA	CCC	CTG	GCC	AGC	AGC	GAG	ACG	230
Cys Arg	Leu Cys	Asn Ile	Pro	Leu	Ala	Ser	Arg	Glu	Thr	
			55	60						
CCT GTC	TGC TAT	GAT CTC	TTT	CAC	TGG	GCC	TGC	CTC	AAT	275
Leu Val	Cys Tyr	Asp Leu	Phe	His	Trp	Ala	Cys	Leu	Asn	
			70	75						
										80

FIGURE 1 (II)

Substitute Sheet (Rule 26)

4/85

CGG TCT "GATTACA"

FIGURE 1 (III)

GCC TCT	GCT GCC	CCA	GCC	TTC	TAC	AGC	CGA	GCC	CCC	CGG	CCC	CCA	590
Ala Ser	Ala Ala	Pro Ala	Pro Ala	Phe	Tyr	Ser	Arg	Ala	Pro	Arg	Pro	Pro	
	175				180					185			
GCT TCC	CCA GGC	CGG	CCC	GAG	CAG	CAC	ACA	GTG	ATC	CAC	ATG	GGC	635
Ala Ser	Pro Gly	Arg Pro	Pro Glu		Gln	His	Thr	Val	Ile	His	Met	Gly	
	190				195					200			
AAT CCT	GAG CCC	TTG	ACT	CAC	GCC	CCT	AGG	AAG	GTG	TAT	GAT	ACG	680
Asn Pro	Glu Pro	Leu Thr	Thr His		Ala	Pro	Arg	Lys	Val	Tyr	Asp	Thr	
	205				210					215			
CGG GAT	GAT GAC	CGG	ACA	CCA	GGC	CTC	CAT	GGA	GAC	TGT	GAC	GAT	725
Arg Asp	Asp Asp	Arg Thr	Thr Pro	Pro	Gly	Leu	His	Gly	Asp	Cys	Asp	Asp	
	220				225					230			
GAC AAG	TAC CGA	CGT	CGG	CCG	GCC	TTG	GGT	TGG	CTG	GCC	CGG	CTG	770
Asp Lys	Tyr Arg	Arg Arg	Arg Pro	Pro	Ala	Leu	Gly	Trp	Leu	Ala	Arg	Leu	
	235				240					245			
CTA AGG	AGC CGG	GCT	GGG	TCT	CGG	AAG	CGG	CCG	CTG	ACC	CTG	CTC	815
Leu Arg	Ser Arg	Ala Gly	Ser	Ser	Arg	Lys	Arg	Pro	Leu	Thr	Leu	Leu	
	250				255					260			

1911 1912 1913 1914 1915 1916 1917 1918 1919 1920 1921 1922 1923 1924 1925 1926 1927 1928 1929 1930 1931 1932 1933 1934 1935 1936 1937 1938 1939 1940 1941 1942 1943 1944 1945 1946 1947 1948 1949 1950 1951 1952 1953 1954 1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2

FIGURE 1 (IV)										860					
CAG	CGG	CGG	CTG	CTG	CTA	CTC	TTG	GGA	CTG	CTG	GGC	TTC	CTG	Leu	
Gln	Arg	Ala	Gly	Leu	Leu	Leu	Leu	Gly	Leu	Leu	Leu	Gly	Phe	Leu	
														275	
														270	
GCC	CTC	CTT	GCC	CTC	ATG	TCT	CGC	CTA	GGC	CGG	GCC	GCA	GCT	GAC	905
Ala	Leu	Leu	Ala	Leu	Met	Ser	Arg	Leu	Gly	Arg	Ala	Ala	Ala	Asp	
														285	
														280	
AGC	GAT	CCC	AAC	CTG	GAC	CCA	CTC	ATG	AAC	CCT	CAC	ATC	CGC	GTG	950
Ser	Asp	Pro	Asn	Leu	Asp	Pro	Leu	Met	Asn	Pro	His	Ile	Arg	Val	
														300	
														305	
														1002	
GCC	CCC	TCC	TGA	GGCCCCCTTGC	TTGTGGCTAG	GCCAGCCTAG	GATGTGGGTT								
Gly	Pro	Ser	*												
														310	
														1052	
CTGTGAGGA	GAGCGGGGT	AATGGGGAGG	CTGAGGGCAC	CTCTTCACTG											
														1102	
CCCCCTCTCCC	TCAAGCCTAA	GACACTAAGA	CCCCAGACCC	AAAGCCAAGT											
														1152	
CCACCAGAGT	GGCTCGCAGG	CCAGGCCTGG	AGTCCCCCGTG	GGTCAAGCAT											

[illegible]

FIGURE 1 (V)				
TTGTCTTGAC	TTGCTTTCTC	CCGGGTCTCC	AGCCTCCGAC	CCCTCGCCCC
1202				
ATGAAGGAGC	TGGCAGGTGG	AAATAAACAA	CAACTTTATT	
1242				

Figure 2

gb|AA155210|AA155210 mr98e01.r1 Stratagene mouse embryonic carc:ncma
(#937317) Mus musculus cDNA clone 505496 5'

Query: : MGLCKCPKRXVTNLFCEHRVNVCEHCLVANHAKCTVQSYLQWLQDSDYNPNCRLCNIPLE
MGLCKCPKRXVTNLFCEHRVNVCEHCLVANHAKCTVQSYLQWLQDSDYNPNCRLCN PL
Sbjct: 38 MGLCKCPKRXVTNLFCEHRVNVCEHCLVANHAKCTVQSYLQWLQDSDYNPNCRLCNTPL 177

8/85

FIGURE 3

dbj|D75913| CELK111G3F C. elegans cDNA clone yk111g3:5' end, single read.

Query:	7	PKRKVTNLF	CFEHRVNVCE	HCLVANHAKCIVQSYLQWLQDSDYNPNCRLCNIPLASRETT	66	
		PKRKVTNLF	+EHRVNVCE	LV NH C+VQSYL WL D DY+PNC LC L +T		
Sbjct:	1	PKRKVTNLF	XYEHRVNVCE	XLVDNHPNCVVQSYLTWLTQDQDYPNCSLCKTTLXEGDTI	180	
Query:	67	RLVCYDL	FWACLN	ERAAQLPRNTAPAGYQCP	98	
		RL C L HW C +E	P	TAP GY+CP		
Sbjct:	181	RLNCLHLL	HWKCFDEWXGNFPD	TTAPXGYRCP	276	
					275	
					PCCSQEVFPDQ	310

9/85

009760" 0544460

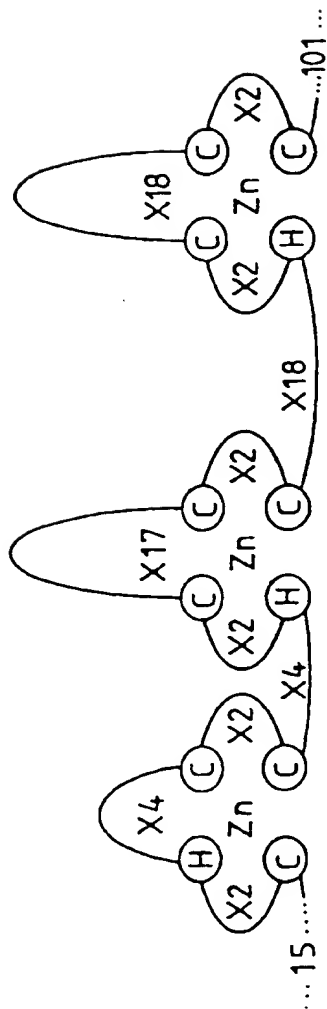


FIG 4

10/85

FIGURE 5

sp | P46580 | YLBS_CAEEL HYPOTHETICAL 146.8 KD PROTEIN C34E10.5 IN
CHROMOSOME III gi|500728 (U10402) C34E10.5 gene product
[Caenorhabditis elegans]

Query: 56 CNIPLASRETTTRLVCYDLFWACLNERRAAQLPRNTAPAGYQCPSC 100
C+I L ++ + L C LF W C+ E A + + + +CP C
Sbjct:1222 CSICLENKNPSALFCGHLFCWTCIQEHAVAATSSASTSSARCPQC 1266

009760" 83442460

11/85

FIGURE 6

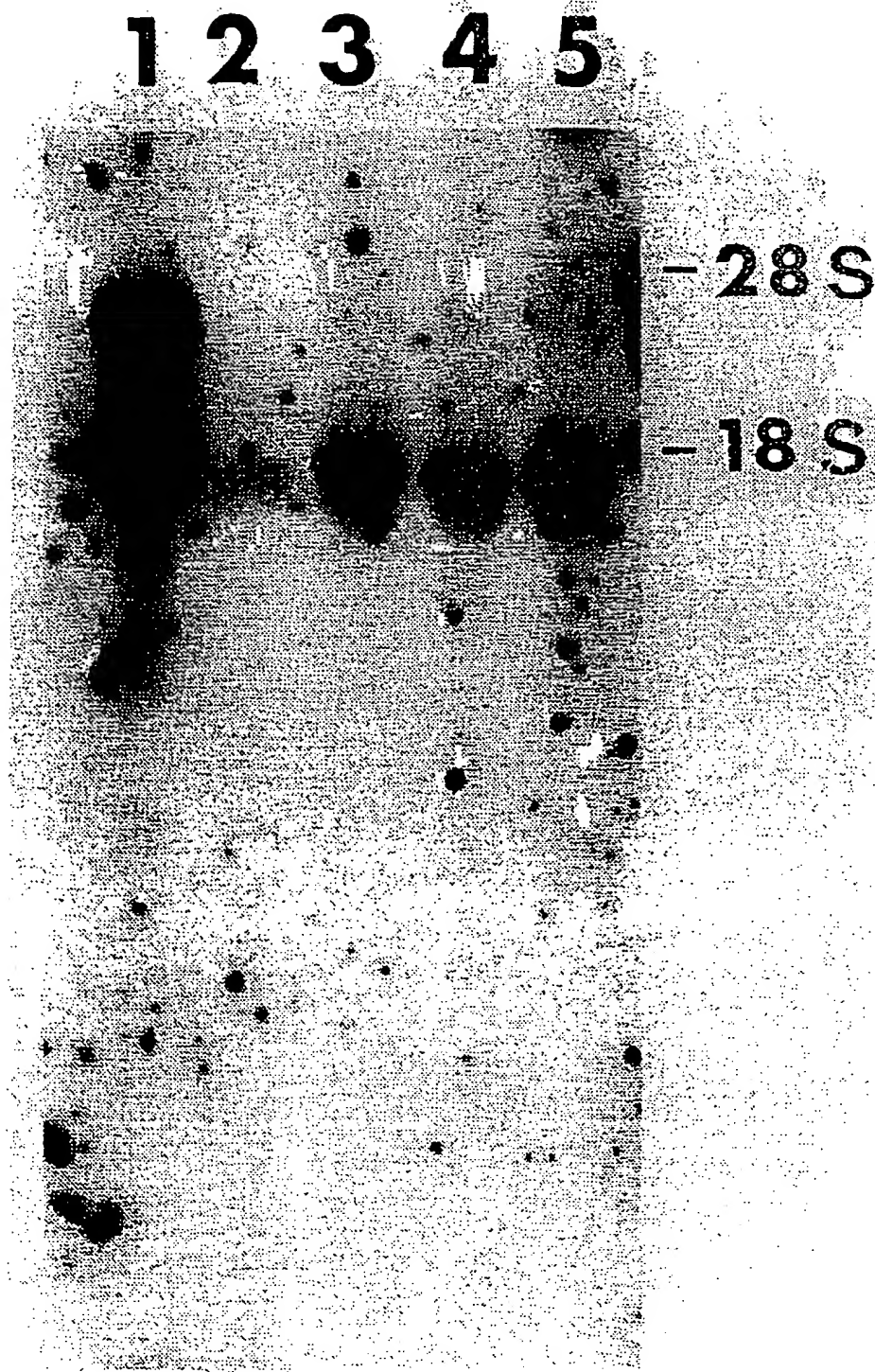
gi | 703468 | (L29051) homologous to GATA-binding transcription factor
[Schizosaccharomyces pombe]

Query: 35 CIVQSYLQWLQDSDYNPNCRLCNI 58
C + +W +D NP C C +
Sbjct: 175 CATNTPKWRRDESGNPICNACGL 198

Query: 162 SSTPGPEEVDASASAAPAFYSQAPRPPASGRPEQHTVIHMGNPEPLTHAPRKVYDTRDDD 221
+S PEE S S S P+ SP+ +Q +I P +V + D
Sbjct: 441 ASLLNPEEPPSNSDKQPSMSNGPKSEVSPSQSQQAFLIQSSTSPVSLQFPPEVQGSNVDK 500

Query: 222 RTPGLH 227
R L+
Sbjct: 501 RNYALN 506

12/85

FIG 7

13/85

FIG 8 (I)FIG 8 (II)FIG 8 (III)FIG 8 (IV)FIG 8 (V)FIG 8 (VI)FIG 8 (VII)FIG 8

14/85

Homo sapiens cDNA clone 531612 5'

Length = 417

Plus Strand HSPs:

Score = 818 (226.0 bits), Expect = 6.1e-103, Sum P(5)=6.1e-103

Identities = 206/259 (79%), Positives = 206/259 (79%), Strand = Plus/Plus

Query: 446 GGCCTCCCTCTGATCGATGAGGTGGTGAGCCCGAGCCCGAGCCCTCAACACGTCCTGAC 505

[illegible]

Sbjct: 49 GGGCTCCCTCTGATCGATGAGGTGATAAGCCCGAGCCCCGAGCCCTCAATTCTCAGAC 108

Query: 506 TTCTCTGACTGGTCTAGTTTTAAATGCCAGCAGTACCCCTGGACCAGAGGAGGTAGACAGC 565

Sbjct: 109 TTCTCTGATTGGTCCAGCTTTAATGCCACCACCCTCTGTGCAAGAGGAGAGAGCCAGC 168

15/85

FIGURE 8 (II)

Query: 566 GCCTCTGCTGCCCCCAGCCCTTCTACAGCCAGGCCCCCGGCCAGCTTCCCCAGGCCGG 625
 Sbjct: 169 ACTCCATCTGCACCTGCTTCTATAGCCAGGCTCCCCCGCCCTCCTCCCTCCCCAAGCCGT 228

Query: 626 CCCGAGCAGCACACAGTGATCCACATGGGCAATCCTGAGCCCTTGACTCACGCCCCCTAGG 685
 Sbjct: 229 CCCGAGCAGCACACAGTCATACACATGGGGAGTACTGAAGCCCTGGCACACGCCCCAAGG 288

Query: 686 AAGGTGTATGATACGCCGG 704
 Sbjct: 289 AAAGTATATGACACACCCGG 307

Score = 230 (63.6 bits), Expect = 6.1e-103, Sum P(5)=6.1e-103
 Identities = 50/55 (90%), Positives = 50/55 (90%), Strand = Plus/Plus

FIGURE 8 (III)

Query: 398 GCACTGAGAGAGAAGCTGGCCACAGTCAACTGGGCCCGGCAGGACTGGGCCTCC 452
 |||||
 Sbjct: 2 GCACTGAGAGAAAGCTAGCCACAGTCAACTGGGCCCGGCAGGACTGGGCCTCC 56

Score = 175 (48.4 bits), Expect = 6.1e-103, Sum P(5) = 6.1e-103
 Identities = 39/44 (88%), Positives = 39/44 (88%), Strand = Plus/Plus

16/85

Query: 767 GCCTTGGGTTGGCTGGCCCCGGCTGCTAAGGAGCCGGGCTGGGTC 810
 |||||
 Sbjct: 373 GCTCTGGGCTGGCTGGCCCCAGCTGCTCAGGAGCCGGGCTGGGTC 416

Score = 139 (38.4 bits), Expect = 6.1e-103, Sum P(5) = 6.1e-103
 Identities = 31/35 (88%), Positives = 31/35 (88%), Strand = Plus/Plus

17/85

FIGURE 8 (IV)

Query: 731 GGAGACTGTGACGATGACAAAGTACCGACGTCGGCC 765
|||||
Sbjct: 336 GGAGACTGTGATGATGACAAATACCGCCCGCGGCC 370

Score = 133 (36.8 bits), Expect = 6.1e-103, Sum P(5)=5.1e-103
Identities = 29/32 (90%), Positives = 29/32 (90%), Strand = Plus/Plus

Query: 701 CGGGATGATGACCGGACACCGAGGCCCTCCATGG 732
|||||
Sbjct: 305 CGGGATGATGACCGGACACCGAGGCATTTCATGG 336

18/85

FIGURE 8 (V)

gb | AA134788 | AA134788 zm81g02.r1 Stratagene neuroepithelium (#937231)
 Homo sapiens cDNA clone 532082 5'
 Length = 368

Plus Strand HSPs:

Score = 563 (155.6 bits), Expect = 3.8e-87, Sum P(3)=3.8e-87
 Identities = 147/190 (77%), Positives = 147/190 (77%), Strand = Plus/Plus

Query: 498 CGTCTGACTTCTCTGACTGGTCTAGTTTAAATGCCAGCAGTACCCCTGGACCAGAGGAGG 557
 |||||
 Sbjct: 103 CCTCAGACTTCTCTGATTGGTCCAGCTTAAATGCCACCACCACCTCTGTGCAAGAGGAGA 162

$\{f_{n,i}\}_{i=1}^{\infty}$ is a sequence of functions in $L^1(\mathbb{R}^n)$ such that $\|f_{n,i}\|_1 \leq 1$ and $\int_{\mathbb{R}^n} f_{n,i} dx \rightarrow 0$ as $n \rightarrow \infty$. Then $\{f_{n,i}\}_{i=1}^{\infty}$ is a sequence of functions in $L^1(\mathbb{R}^n)$ such that $\|f_{n,i}\|_1 \leq 1$ and $\int_{\mathbb{R}^n} f_{n,i} dx \rightarrow 0$ as $n \rightarrow \infty$.

FIGURE 8 (VI)

```

Query: 558 TAGACAGCGCCTCTGCTGCCCCAGCCTTCTACAGCCAGGCCCCCGGCCCCAGCTTCCC 617
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 163 GAGCCAGCACTCCATCTGCGCCTGCTTCTATAGCCAGGCTCCCCGCCCTCCTCCCTCCC 222

```

Query: 618 CAGCCGCCCGAGCAGCACACAGTGATCCACATGGCAATCTGAGCCCCTTACTCACC 677
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 223 CAAGCCGTCCCGAGCAGCACACAGTCATACACATGGGGAGTACTGAAGCCCCCTGGCACACG 282

```

Query: 678 CCCCTAGGAA 687
      |||||
Sbjct: 283 CCCCAGGAA 292

```

Score = 454 (125.4 bits), Expect = 3.8e-87, Sum P(3) = 3.8e-87
Identities = 94/98 (95%), Positives = 94/98 (95%), Strand = Plus/Plus

20/85

FIGURE 8 (VII)

Query: 398 GCACTGAGAGAGAAAGCTGGCCACAGTCAACTGGGCCCGGCGAGGACTGGGCTCCCTCTG 457
 |||||
 Sbjct: 2 GCACTGAGAGACAAGCTAGCCACAGTCAACTGGGCCCGGCGAGGACTGGGCTCCCTCTG 61

Query: 458 ATCGATGAGGTGGTGAGCCCCAGAGCCCCGAGCCCCCTCAA 495
 |||||
 Sbjct: 62 ATCGATGAGGTGATAAGCCACAGAGCCCCGAGCCCCCTCAA 99

Score = 219 (60.5 bits), Expect = 3.8e-87, Sum P(3) = 3.8e-87
 Identities = 51/60 (85%), Positives = 51/60 (85%), Strand = Plus/Plus

Query: 702 GGGATGATGACCCGACACACAGGCCCTCCATGGAGACTGTGACGATGACAAAGTACCGACGTC 761
 |||||
 Sbjct: 309 GGATTGATGACCCGACAGCAGGCATTTCATGGAGACTGTGATGATGACAAATACCGCCGCC 368

FIGURE 9

W32939 human

TACCGCCCTTCGGAACCCAGTGCAGCGGCCGATCAGTAAACACAGAGACTGGGATCGATCATGGGGCTTTGTAAAG

AA242159 mouse

CTTCCGGCGCTTTTTCATTACCGTACGCACCGGTCA-CGATCGGCATCGCGGAGGATCGGTCAATGGGACTTTTGCAAG

21/85

22/85

FIG 10 (I)FIG 10 (II)FIG 10 (III)FIG 10 (IV)FIG 10

23/85

5.

[74]

*****^

	130	140	150	160	170	180
MCG4	*	*	*	*	*	*
	KLATVNWARA	GLGLPLIDEV	VSPEPEPLNT	SDFS DWSSFN	ASSTPGPEEV	DSASAAPAFY
1.	20	30	40	50	60	
[372]	*****	i*****s	*****	*tt*svq**r	a*tps*****>	
2.	30	40	50	60		
[243]	_____aq s*s*sip	*****	*tt*svq**r	a*tps*****>		
						*p
3.	10	20	30	40	50	60
[229]	*****	*****i*****s	xrll*lvql*	chhhlcarge	sqh*icac*l>	

24/85

FIGURE 10 (II)

```

s |
||
||
10      30      40      50      60 |
[ 74 ] ***** q**s*-sipq tslig-pal- mppp*lcrr ep*hlhlli>

MCG4  SRAPRPPASP GRPEQHTVIH MGNPEPLTHA PRKVDYDTRDD DRTPGLHGDC DDDKYRRRPA
      190      200      210      220      230      240
      *      *      *      *      *      *
      SRAPRPPASP GRPEQHTVIH MGNPEPLTHA PRKVDYDTRDD DRTPGLHGDC DDDKYRRRPA
      **

1.      70      80      90      100      110      120
[ 372 ] *q*****p** s***** **st*a*a** *****pgp *srhswetvm mtnt-aagl*>

2.      70      80      90
[ 243 ] *q*****p** s***** **st*a*a** ***>

i
|
3.      70      80      90      100      110      120
[ 229 ] gsp*sslpk* s*a-a*sht* gey*s*g*r- *kek*m*hg* ****a*i*****>

4.      70      80      90      100      110      120
[ 86 ]  _p*sslpk* s*a-a*sht* gey*s*g*rp kesi*h*gmm tggqafm*** *****c>

h

```


25/85

FIGURE 10 (III)

5. [74] arl*allppq av*sstqsy t w*vlk*w-*t *qgk*m***** **a*i**>

g

6. [38] _____ *t *q*****>

MCG4 1. 130 250 * LGWLARLLRS RAGSRKRPLT LLQRAGLLLL LGLLGLFALL ALMSRLGRAA ADSDPNLDPL
260 * 270 * 280 * 290 * 300 *

[372] *****q***** **>

4.

[86] S*-*>

310

*

MCG4 MNPHIRVGPS

26/85

FIGURE 10 (IV)

Search Analysis for Sequence: MCG4

Search from 1 to 310

Date: September 22, 1997

Matrix: pam250 matrix

Score Region from 1 to 310

Maximum possible score: 1598

Aligned sequences:

1. = EST AA074703 phase 1 translation
2. = EST AA134788 phase 3 translation
3. = EST AA134788 phase 2 translation
4. = EST AA074703 phase 3 translation
5. = EST AA074703 phase 2 translation
6. = EST AA134788 phase 1 translation

0037E0"85ttt60

Domains of MCG4

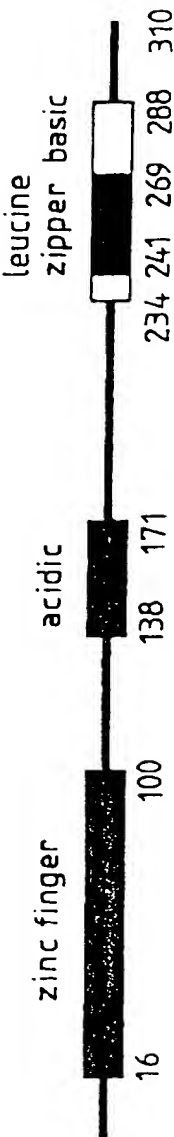


FIGURE 11

zinc finger consensus: CX₂HXCX₂CX₄HXCX₂CX₁₇CX₂CX₁₈HXCX₁₈CX₂C

acidic domain consensus: 9/34 negatively charged amino acids, 0/34 positively charged

basic domain consensus: 13/55 positively charged amino acids, 0/55 negatively charged

leucine zipper domain consensus: LX₆LX₆RX₆LX₆L

alternate "novel" leucine zipper-like motif where leucine would not be aligned along the one surface of an alpha helix domain: (aa 261) LX₆LXLX₆LXLX₆L (aa 286)

27/85

28/85

<u>FIG 12 (I)</u>	<u>FIG 12 (II)</u>
<u>FIG 12 (III)</u>	<u>FIG 12 (IV)</u>

FIG 12

29/85

FIG 12 (I)

Sequences producing High-scoring Segment Pairs:

gn1 PID e236178	(Z70752 F25B3.3 [Caenorhabditis ele...
gi 1293099	(U53884) aimless RasGEF [Dictyosteli...
gi 1655941	(U67326) Ras-GRF2 [Mus musculus]
pir s30356	CDC25 protein homolog - yeast (Cand...
sp P43069 CC25_CANAL	CELL DIVISION CONTROL PROTEIN 25
sp P28818 GNRP_RAT	GUANINE NUCLEOTIDE RELEASING PROTEIN...
prf 1814463A	guanine nucleotide-releasing factor ...
pir B46199	nucleotide-exchange-factor homolog c...
gn1 PID e238680	(X97560) hypothetical protein L1309 ...
pir s22693	CDC25 protein homolog - mouse/gi 50...
sp P14771 SC25_YEAST	SCD25 PROTEIN /gi 457494 (M26647) SD...
sp P26674 STE6_SCHPO	STE6 PROTEIN /pir s28098 ste6 prote...
pir s28407	CDC25 protein homolog - mouse
sp P27671 GNRP_MOUSE	GUANINE NUCLEOTIDE RELEASING PROTEIN...
gi 386047	(s62035) Ras-specific guanine nucleo...
sp Q02342 CC25_SACKL	CELL DIVISION CONTROL PROTEIN 25 /pi...
pir s14177	SCD25 protein - yeast (Saccharomyces...
gi 433720	(L26584) CDC25 [Homo sapiens]
gn1 PID e241744	(Z68880) T14G10.2 [Caenorhabditis el...
gi 3484	(X03579) CDC25 protein (aa 1-1588) [...

30/85

009TE0" 00000000

High Score	smallest Sum Probability P(N)	N
307	3.0e-124	8
202	7.8e-22	5
152	3.6e-16	4
150	2.2e-15	3
150	2.2e-15	3
166	2.6e-15	3
166	2.6e-15	3
167	1.1e-14	1
158	3.0e-14	3
167	3.7e-14	2
158	4.6e-14	3
160	5.2e-14	2
167	1.2e-13	3
167	1.2e-13	3
153	2.0e-13	2
142	4.5e-13	2
152	5.7e-13	3
153	6.0e-13	3

FIG 12 (II)

31/85

sp PO4821 CC25_YEAST	CELL DIVISION CONTROL PROTEIN 25 /pi...
gi 915328	(U24070) Munc13-1 [Rattus norvegicus]
pir A46199	nucleotide-exchange-factor homolog c...
pdb 1PTR	Molecule: Protein Kinase C Delta Ty...
gi 915330	(U24071) Munc13-2 [Rattus norvegicus]
gi 474982	(D21239) 'C3G protein' [Homo sapiens]
gi 1763306	(U75361) Munc13-3 [Rattus norvegicus]
gi 806957	guanine-nucleotide exchange factor C...
sp Q03385 GNDS_MOUSE	GUANINE NUCLEOTIDE DISSOCIATION STIM...
pir BVBYL1	LTE1 protein - yeast (Saccharomyces...
gi 452242	(D21354) a putative guanine nucleoti...
sp P07866 LTE1_YEAST	LOW TEMPERATURE ESSENTIAL PROTEIN /P...
gi 509050	(Z22521) protein kinase C delta [Hom...
gi 520587	(D10495) protein kinase C delta-type...
sp P05130 KPC1_DROME	PROTEIN KINASE C, BRAIN ISOZYME (PKC...
pir S35704	protein kinase C (EC 2.7.1.-) delta...
sp Q05655/KPCD_HUMAN	PROTEIN KINASE C, DELTA TYPE (NPKC-D...
pir S40279	protein kinase C mu - human /pir A5...
sp P09215 KPCD_RAT	PROTEIN KINASE C, DELTA TYPE (NPKC-D...
gi 520878	(Z34524) serine/threonine protein ki...
gi 1519719	(U68142) RalGDS-like [Homo sapiens]

FIG 12 (III)

32/85

$$\begin{array}{ccccccc} \Gamma_{\text{red}}^{(1)} & \Gamma_{\text{red}}^{(2)} & \Gamma_{\text{red}}^{(3)} & \Gamma_{\text{red}}^{(4)} & \Gamma_{\text{red}}^{(5)} & \Gamma_{\text{red}}^{(6)} & \Gamma_{\text{red}}^{(7)} \\ \Gamma_{\text{red}}^{(1)} & \Gamma_{\text{red}}^{(2)} & \Gamma_{\text{red}}^{(3)} & \Gamma_{\text{red}}^{(4)} & \Gamma_{\text{red}}^{(5)} & \Gamma_{\text{red}}^{(6)} & \Gamma_{\text{red}}^{(7)} \end{array}$$

FIG 12 IV

7.2e-13	1
3.4e-12	3
3.4e-12	3
5.5e-12	1
5.6e-12	1
1.5e-11	1
1.6e-11	2
3.3e-11	3
6.4e-11	2
7.8e-11	3
1.0e-10	2
1.9e-10	1
2.7e-10	1
2.7e-10	1
4.0e-10	1
4.6e-10	1
4.7e-10	1
4.7e-10	1
4.7e-10	1
4.9e-10	1
9.0e-10	1
1.8e-09	1
3.8e-09	3

157
136
136
151
149
136
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153
128
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135
133
115

33/85

FIG 13a (I)FIG 13a (II)FIG 13a (III)FIG 13a (IV)FIG 13a (V)FIG 13a (VI)FIG 13a (VII)FIG 13a (VIII)FIG 13a (IX)FIG 13a (X)FIG 13a

34/85

FIGURE 13(a) (I)

CG ATT	TCA	TTC	CTC	GCT	CCC	CAC	AGG	TCC	CTC	TCC	CCA	AAA	TAT	44
Ile	Ser	Phe	Leu	Ala	Pro	His	Arg	Ser	Leu	Ser	Pro	Lys	Tyr	
1				5					10					
TCC	CAT	CTT	GTC	CTA	GCC	CAT	CCC	CCA	GAC	TAT	CTC	AAG	GAC	CAG
Ser	His	Leu	Val	Leu	Ala	His	Pro	Pro	Asp	Tyr	Leu	Lys	Asp	Gln
15				20					25					89
CTG	TCC	CCA	CGC	CCC	CGA	CCT	CCA	CTA	GGC	CTG	TGC	CAC	CCG	CTG
Leu	Ser	Pro	Arg	Pro	Arg	Pro	Pro	Leu	Gly	Leu	Cys	His	Pro	Leu
30				35					40					134
CCT	GCA	GGA	AGA	CGC	CCG	GTC	CCG	GGC	CGG	GTT	AGC	CCC	ATG	GGA
Pro	Ala	Gly	Arg	Arg	Pro	Val	Pro	Gly	Arg	Val	Ser	Pro	Met	Gly
45				50					55					179
ACG	CAG	CGC	CTG	TGT	GGC	CGC	GGG	ACT	CAA	GGC	TGG	CCT	GGC	TCA
Thr	Gln	Arg	Leu	Cys	Gly	Arg	Gly	Thr	Gln	Gly	Trp	Pro	Gly	Ser
60				65					70					224
AGT	GAA	CAG	CAC	GTC	CAG	GAG	GCG	ACC	TCG	TCC	GCG	GGT	TTG	CAT
Ser	Glu	Gln	His	Val	Gln	Glu	Ala	Thr	Ser	Ser	Ala	Gly	Leu	His
75				80					85					269

35/85

FIGURE 13(a) (II)															
TCT	GGG	GTG	GAC	GAG	CTG	GGG	GTT	CGG	TCC	GAG	CCC	GGT	GGG	AGG	314
Ser	Gly	Val	Asp	Glu	Leu	Gly	Val	Arg	Ser	Glu	Pro	Gly	Gly	Arg	
90					95					100					
CTC	CCG	GAG	CGC	AGC	CTG	GGC	CCA	GCC	CAC	CCC	GGC	CCG	GGC	GCC	359
Leu	Pro	Glu	Arg	Ser	Leu	Gly	Pro	Ala	His	Pro	Ala	Pro	Ala	Ala	
105					110					115					
ATG	GCA	GGC	ACC	CTG	GAC	CTG	GAC	AAG	GGC	TGC	ACG	GTG	GAG	GAG	404
Met	Ala	Gly	Thr	Leu	Asp	Leu	Asp	Lys	Gly	Cys	Thr	Val	Glu	Glu	
120					125					130					
CTG	CTC	CGC	GGG	TGC	ATC	GAA	GCC	TTC	GAT	GAC	TCC	GGG	AAG	GTG	449
Leu	Leu	Arg	Gly	Cys	Ile	Glu	Ala	Phe	Asp	Asp	Ser	Gly	Lys	Val	
135					140					145					
CGG	GAC	CCG	CAG	CTG	GTG	CGC	ATG	TTC	CTC	ATG	ATG	CAC	CCC	TGG	494
Arg	Asp	Pro	Gln	Leu	Val	Arg	Met	Phe	Leu	Met	Met	His	Pro	Trp	
150					155					160					
TAC	ATC	CCC	TCC	TCT	CAG	CTG	GCG	GCC	AAG	CTG	CTC	CAC	ATC	TAC	539
Tyr	Ile	Pro	Ser	Ser	Gln	Leu	Ala	Ala	Lys	Leu	Leu	His	Ile	Tyr	
165					170					175					

36/85

FIGURE 13(a) (III)

CAA CAA TCC CGG AAG	GAC AAC TCC AAT TCC CTG CAG GTG AAA ACG	584
Gln Gln Ser Arg Lys	Asn Ser Asn Ser Leu Gln Val Lys Thr	190
180		
TGC CAC CTG GTC AGG	TAC TGG ATC TCC GCC TTC CCA GCG GAG TTT	629
Cys His Leu Val Arg	Trp Ile Ser Ala Phe Pro Ala Glu Phe	200
195		
GAC TTG AAC CCG GAG	TTG GCT GAG CAG ATC AAG GAG CTG AAG GCT	674
Asp Leu Asn Pro Glu	Leu Ala Glu Gln Ile Lys Glu Leu Lys Ala	215
210		
CTG CTA GAC CAA GAA GGG	AAC CGG CAC AGC AGC CTA ATC GAC	719
Leu Leu Asp Asn Gln Glu	Gly Asn Arg Arg His Ser Ser Leu Ile Asp	230
225		
ATA GAC AGC GTC CCT	ACC TAC AAG TGG AAG CGG CAG GTG ACT CAG	764
Ile Asp Ser Val Pro	Thr Tyr Lys Trp Lys Arg Arg Val Thr Gln	245
240		
CGG AAC CCT GTG GGA	CAG AAA AAG CGC AAG ATG CTG TTG TTT	809
Arg Asn Pro Val Gly	Gln Lys Arg Lys Met Ser Leu Leu Phe	260
255		

Journal of Management Studies, 19(6), 701-718.

GAC Asp 270	CAC His	CTG Leu	GAG Leu	ATG Met 275	GAG Glu	CTG Leu	GCG Ala	GAG Glu	CAT His 280	CTC Leu	ACC Thr	TAC Tyr	TTG Leu	854
GAG Glu 285	TAT Tyr	CGC Arg	TCC Ser	TTC Phe	TGC Cys 290	AAG Lys	ATC Ile	TTT Phe	CAG Gln 295	GAC Asp	TAT Tyr	CAC His	AGT Ser	899
TTC Phe 300	GTG Val	ACT Thr	CAT His	GGC Gly	TGC Cys 305	ACT Thr	GTG Val	AAC Asn	CCC Pro 310	GTC Val	CTG Leu	GAG Glu	CGG Arg	944
TTC Phe 315	ATC Ile	TCC Ser	CTC Leu	TTC Phe	AAC Asn 320	AGC Ser	GTG Val	CAG Gln	TGG Trp 325	GTG Val	CAG Gln	CTC Leu	ATG Met	989
ATC Ile 330	CTC Leu	AGC Ser	AAA Lys	CCC Pro	ACA Thr 335	GCC Ala	CCG Pro	CGG Arg	GCC Ala 340	CTG Leu	GTC Val	ATC Ile	ACA Thr	1034

38/85

CCTC "CCTC" C

FIGURE 13(a) (V)

CAC TTT GTC CAC GTG GCG GAG AAG CTG CTA CAG CTG CAG AAC TTC	1079
His Phe Val His Val Ala Val Val Val Val Val Val Val Val Val	345
AAC ACG CTG ATG GCA GTG GTC GGG GGC CTG AGC CAC AGC TCC ATC	1124
Asn Thr Leu Met Ala Val Val Val Val Val Val Val Val Val	360
TCC CGC CTC AAG GAG ACC CAC AGC AGC GTT AGC CCT GAG ACC ATC	1169
Ser Arg Leu Lys Lys Glu Thr Thr Thr Thr Thr Thr Thr Thr	375
AAG CTC TGG GAG GGT CTC CTC ACG GAA CTA GTG ACG GCG ACA GGC AAC	1214
Lys Leu Trp Glu Glu Thr Thr Thr Thr Thr Thr Thr Thr Thr	390
TAT GGC AAC TAC CGG CGT CGG CTG GCA GCC TGT GTG GGC TTC CGC	1259
Tyr Gly Asn Tyr Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg	405
TTC CCG ATC CTG GGT GTG CAC CTC AAG GAC CTG GTG GCC CTG CAG	1304
Phe Pro Ile Leu Gly Val Val Val Val Val Val Val Val Val	420

39/85

FIGURE 13(a) (VI)

CTG GCA CTG CCT GAC	TGG	CTG	GAC	CCA	GCC	CGG	ACC	CGG	CTC	AAC	1349
Leu Ala Leu Pro Asp	Trp	Leu	Asp	Pro	Ala	Arg	Thr	Arg	Leu	Asn	
435	440					445					
GGG GCC AAG ATG AAG	CAG	CTC	TTT	AGC	ATC	CTG	GAG	GAG	CTG	GCC	1394
Gly Ala Lys Met Lys	Gln	Leu	Phe	Ser	Ile	Leu	Glu	Glu	Leu	Ala	
450	455					460					
ATG GTG ACC AGC CTG	CGG	CCA	CCA	GTA	CAG	GCC	AAC	CCC	GAC	CTG	1439
Met Val Thr Ser Leu	Arg	Pro	Pro	Val	Gln	Ala	Asn	Pro	Asp	Leu	
465	470					475					
CTG AGC CTG CTC ACG	GTG	TCT	CTG	GAT	CAG	TAT	CAG	ACG	GAG	GAT	1484
Leu Ser Leu Leu Thr	Val	Ser	Leu	Asp	Gln	Tyr	Gln	Thr	Glu	Asp	
480	485					490					
GAG CTG TAC CAG CTG	TCC	CTG	CAG	CGG	GAG	CCG	CGC	TCC	AAG	TCC	1529
Glu Leu Tyr Gln Leu	Ser	Leu	Gln	Arg	Glu	Pro	Arg	Ser	Lys	Ser	
495	500					505					

1. *Staphylococcus aureus* (S. aureus) is a Gram-positive, spherical bacterium that is commonly found on the skin and in the nose of humans and animals. It is a facultative anaerobe, meaning it can grow with or without oxygen. S. aureus is known for its ability to form a thick, protective layer called a biofilm, which can make it difficult to treat with antibiotics.

TCG Ser 510	CCA Pro	ACC Thr	AGC Ser	CCC Pro	ACG Thr	AGT Ser	TGC Cys	ACC Thr	CCA Pro	CCA Pro	CCC Pro	CGG Arg	CCC Pro	CCG Pro	1574
GTA Val 525	CTG Leu	GAG Glu	GAG Glu	TGG Trp	ACC Thr	TCG Ser	GCT Ala	GCC Ala	AAA Lys	CCC Pro	AAG Lys	CTG Leu	GAT Asp	CAG Gln	1619
GCC Ala 540	CTC Leu	GTG Val	GTG Val	GAG Glu	CAC His	ATC Ile	GAG Glu	AAG Lys	ATG Met	GTG Val	GAG Glu	TCT Ser	GTG Val	TTC Phe	1664
CGG Arg 555	AAC Asn	TTT Phe	GAC Asp	GTC Val	GAT Asp	GGG Gly	GAT Asp	GGC Gly	CAC His	ATC Ile	TCA Ser	CAG Gln	GAA Glu	GAA Glu	1709
TTC Phe 570	CAG Gln	ATC Ile	ATC Ile	CGT Arg	GGG Gly	AAC Asn	TTC Phe	CCT Pro	TAC Tyr	CTC Leu	AGC Ser	GCC Ala	TTT Phe	GGG Gly	1754
GAC Asp 585	CTC Leu	GAC Asp	CAG Gln	AAC Asn	CAG Gln	GAT Asp	GGC Gly	TGC Cys	ATC Ile	AGC Ser	AGG Arg	GAG Glu	GAG Glu	ATG Met	1799

41/85

FIGURE 13(a) (VIII)

GTT TCC TAT TTC CTG	CGC TCC AGC TCT GTG TTG GGG GGC CGC ATG	1844
Val Ser Tyr Phe Leu	Arg Ser Ser Val Leu Gly Gly Arg Met	610
600	605	
GGC TTC GTA CAC AAC TTC	GAG AGC AAC TCC TTG CGC CCC GTC	1889
Gly Phe Val His Asn	Gln Glu Ser Asn Ser Leu Arg Pro Val	625
615	620	
GCC TGC CGC CAC TGC	AAA GCC CTG ATC ATC GGC ATC TAC AAG CAG	1934
Ala Cys Arg His Cys	Lys Ala Leu Ile Leu Gly Ile Tyr Lys Gln	640
630	635	
GGC CTC AAA TGC CGA	GCC GGA GTG AAC TGC CAC AAG CAG TGC	1979
Gly Leu Lys Cys Arg	Ala Cys Gly Val Asn Cys His Lys Gln Cys	655
645	650	
AAG GAT CGC CTG TCA	GTT GAG TGT CGG CGC AGG GCC CAG AGT GTG	2024
Lys Asp Arg Leu Ser	Val Glu Cys Arg Arg Ala Gln Ser Val	665
660	670	

42/85

003700" 05111100

FIGURE 13(a) (IX)

AGC CTG GAG GGG TCT	GCA CCC TCA CCC ATG CAC AGC CAC	2069
Ser Leu Glu Gly Ser	Ala Pro Ser Pro Met His Ser His	
675	680	685
CAT CAC CGC GCC TTC AGC	TTC TCT CTG CCC CGC CCT GGC AGG CGA	2114
His His Arg Ala Phe	Ser Phe Ser Leu Pro Arg Pro Gly Arg Arg	
690	695	700
GGC TCC AGG CCT CCA GAG	ATC CGT GAG GAG GTA CAG ACG GTG	2159
Gly Ser Arg Pro Pro	Glu Ile Arg Glu Glu Val Gln Thr Val	
705	710	715
GAG GAT GGG GTG TTT GAC	ATC CAC TTG TA ATAGATGCTG	2198
Glu Asp Gly Val Phe	Asp Ile His Leu *	
720	725	
TGGTTGGATC AAGGACTCAT	TCCTGCCCTTG GAGAAAATAC TTCAACCAGA	2248
GCAGGGAGCC TGGGGGTGTC	GGGGCAGGAG GCTGGGGGATG GGGGTGGGAT	2293
ATGAGGGTGG CATGCAGCTG	AGGGCAGGGC CAGGGCTGGT GTCCCTAAGG	2348

43/85

FIGURE 13(a) (X)

TTGTACAGAC TCTTGTGAAT ATTTGTATTT TCCAGATGGA ATAAAAGGC	2398
CCGTGTAATT AACCTTC (A)n	2416

09/424458

44/85

FIGURE 13(b)

CGATTTCATT CCTCGCTCCC CACAGGTCCC TCTCCCCAAA ATATTCCCAT 50
 CTTGTCTCTAG CCATATCCCC AGACTATCTC AAGGACCAGC TGTCCCCACG 100
 CCCCCGACCT CCACTAGGCC TGTGCCACCC GCTGCCCTGCA GGAAGACGCC 150
 CCGTCCCCGGG CCGGGTTAG CCC CAT GGG AAC GGG GTT CGG TCC GAG 196
 * Pro His Gly Asn Gly Val Arg Ser Glu
 1 5
 CCC GGT GGG AGG CTC CCG GAG CGC AGC CTG GGC CCA GCC CAC 238
 Pro Gly Gly Arg Leu Pro Glu Arg Ser Leu Gly Pro Ala His
 10 15 20
 CCC GCG CCG GCG GCC ATG GCA GGC ACC CTG GAC CTG GAC AAG 280
 Pro Ala Pro Ala Ala Met Ala Gly Thr Leu Asp Leu Asp Lys
 25 30 35
 GGC TGC ACG GTG GAG GAG CT
 Gly Cys Thr Val Glu Glu Leu
 40 300

45/85

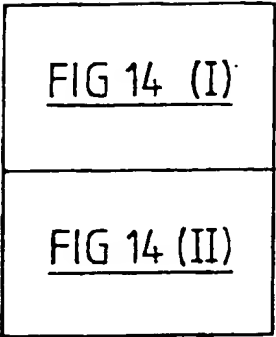


FIG 14 (I)

FIG 14 (II)

FIG 14

46/85

FIGURE 14 (I)

1	MAGTLDDKGC...TVEELLRGCI EAF..DDSGKV RDPQLVRMFLMMHPW	45
1	MSSKVEEDQH QELLTEDQLVARC VECFDVDEEDEDIEFVDALFLSHQW	50
46	YIPSSQLAAKLLHIYQQSRKDNSLSLQVKTCHLVRYWISAFPAEFDLNPE	95
51	LSDSLSLITHFVN FYQETRNV EQRE...AVCRAVSFWIEKFPMHFDAQPQ	97
96	LAEQIKELKALLDQEGNRRHSSLLIDIDSVPTYKWK RQVTQRNPVGQKK..	143
98	VCAQVVRLLKTI AEDINENIRNGL.DVSALPSFAWLRAVSVRNPLAKQTIV	146
144RKMSLLFDHLEPMELAEHLTYLEYR	168
147	RVDFETLPTPGTPPPPIASKKFSLTAFSLSFVQASPSDISTLSL SHIDYR	196
169	SFCKILFQDYHSFVTHGCTVDNPNVLERFISLFNSVSQWVQLMILSKPTAP	218
197	VLSTISITELKQYVKDGH LRS CPMLERSISVFNNLSNWVQCLILNKTTPK	246
219	QALVITHFVHVAEKLLOLONENTLMAVGGLSHSSISR LKETHSHVSPE	268
247	ERAEILVKFVHVAKHLRKINNENTLMSVVGGIT HSSVARLAKTYAVLSND	296
269	TIKLWEGLT ELVTATGNYGN YRRRLAAC.VGFRFPILGVHLKDLVALQLA	317
297	IKKELTQLTNLLSAQHNFCEYRKALGACNKKFRIP IIGVHLKDLVAINCS	346

47/85

FIGURE 14 (II)

318	LPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPV.QANPDLLSLTV	366
347	GANFEKT..KCISSDKLVKLSKLLSNFLVFNQKGHNLPENMDLINTLKV	394
367	SLDQYQTEDELYQLSLQREPRSKSSPTSCTPPPRPPVLEEWTSAKP	416
395	SLDIRYNDDDIYELSLRREPCTFMN.....FEPGRGLVFAEWASGVTV	437
417	KLDQALVVEHIEKMVESVFRNFDVDGDGHIISOEEFQIIRGNFPYLSAFGD	466
438	APDNATVSKHISAMVDAVFKHYDHD RDGFIISOEEFQIIRGNFPYLSAFGD	487
467	LDONODGCISREEMVSYFLRSS.SVLGGRMGFVHNFOESNLRPVACRHC	515
488	IDVDMGQISKDELKTYFMAANKNTKDLRRGFKHNFHETTELTPPTCNHC	537
516	KALILGIYKOGKCRACGVNCHKOCKDRLSVECRRRRAQSVSLEGSAPSPS	565
538	NKLLWGILROGEKCKDCGLAVHSCCKSNAVAECRRKSSSNLTRAAEWFAS	587
566	PMHSHHHRAFSFSLPRPGRRGSRPPEIRREEVQTVEDGVFDIHL	609
588	PRGSMRSRIINTC...NNSGSTPDEEIGLVSLACEEVFEDDDL	627

48/85

FIG 15 (I)

FIG 15 (II)

FIG 15

FIGURE 15 (I)

human	CGATTTCATT	CCTCGCTCCC	CACAGGTCCC	TCTCCCCAAA	ATATTCCCAT	CTTGTCCTAG	60
human	CCCATCCCCC	AGACTATCTC	AAGGACCAGC	TGTCCCCCAG	CCCCCGACCT	CCACTAGGCC	120
human	TGTGCCACCC	GCTGCCCTGCA	GGAAGACGCC	CGGTCCCGGG	CCGGTTAGC	CCCATGGGAA	180
human	CGCAGCGCCT	GTGTGGCCCG	GGGACTCAAG	GCTGGCCTGG	CTCAAGTGAA	CAGCACGTCC	240
mouse			***tcag**	***ag***	t*****	***a*g***t>	
human	AGGAGGCGAC	CTCGTCCGG	GGTTTGCATT	CTGGGGTGGA	CGAGCTGGGG	GTTCGGTCCG	300

acagg

49/85

mouse	g****t**a	**-*catt**	*****	***aa**aa*	g**ct*****	**a**aat**>
human	AGCCCGGTGG	GAGGCTCCCC	GAGCGCAGCC	TGGGCCCAGC	CCACCCCGCG	CCGGCGGCCA
mouse	***a*t***	*****tga	***t*t*a*t	***t*t***	***-*tg**a	***a***>
human	TGGCAGGCAC	CCTGGACCTG	GACAAGGCT	GCACGGTGGA	GGAGCTGCTC	CGCGGGTGCA
mouse	***g****	t*****	*****t*	***c*****	*****	**t**c**t**>
human	TCGAAGCCTT	CGATGACTCC	GGGAAGGTGC	GGGACCCGCA	GCTGGTGCGC	ATGTTCCCTCA

FIGURE 15 (II)

mouse	*****	t*****	**a*****	*a**t**a**	***a*****	*****t*****>
human	TGATGCACCC	CTGGTACATC	CCCTCCTCTC	AGCTGGCGGC	CAAGCTGCTC	CACATCTACC 540
mouse	*****	*****a	**t*****	*****tt*	g**a*****	***t*****t**>
human	AACAATCCCG	GAAGACAAC	TCCAATTCCC	TGCAGGTGAA	AACGTGCCAC	CTGGTCAGGT 600
mouse	*g*****	*****	*****t*	*a**a*****	*****t**	t*****t**>
human	ACTGGATCTC	CGCCTTCCCA	GCGGAGTTTG	ACTTGAACCC	GGAGTTGGCT	GAGCAGATCA 660
mouse	*****	a*****	**a*****c*	*****	a**c*****	***a*****t**>
human	AGGAGCTGAA	GGCTCTGCTA	GACCAAGAAG	GGAACCGACG	GCACAGCAGC	CTAATCGACA 720
mouse	*****	*****t**	*****	*****ca*	*****	**c*****t**>
human	TAGACAGCGT					
mouse	*c**g**t**					

730

51/85

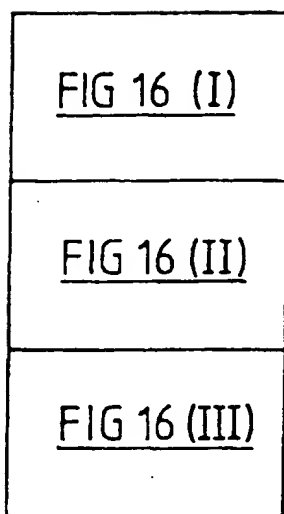


FIG 16

52/85

FIGURE 16 (I)

CACGCCTCGG	AAGGAGGTT	TGGGGTCGGT	GGTTCACAG	TGAGTGTGC	50
TGAAGCCAAA	TGGTCGGAAA	CCGTACCCG	CTCTCCTAG	GCC CGG CTA	98
			* Ala Arg Leu		
GTG GGG ACC CCA ACC GCC	TGC GGC TGC CCC	TCC CAA GTT CCT			140
Val Gly Thr Pro Thr Ala	Cys Gly Cys Pro Ser Gln Val	Pro			
					15
CCC TGT TGG CCA CCA CCA	ATC GGC GTC CAG GTC	TCC AGT CTC CGA GCT GCG			182
Pro Cys Trp Pro Gly Ile	Gln Val Ser Ser Leu Arg	Ala Ala			
					30
GAG AAC CCA CCG CCA CCA	CAT GCG GCT GGC CCT	TTC CAT TCG ACC			224
Glu Asn Pro Pro Pro Pro	His Ala Ala Pro Phe His Ser	Thr			
					45
CTG TGG GGA GCC AGG CTT	CCG GGG CCC CGT TCC	TCC TGT GTG			266
Leu Trp Gly Ala Arg	Pro Gly Pro Arg Ser Ser	Cys Val			
					55
AAC TGG GCC CCC CGC CCC	CAT TCC CAG ACA TCA	AGG CCG CGT			308
Asn Trp Ala Pro Arg	Pro His Ser Gln Thr Ser Arg	Pro Arg			
					65
					70
					70

53/85

FIGURE 16 (II)

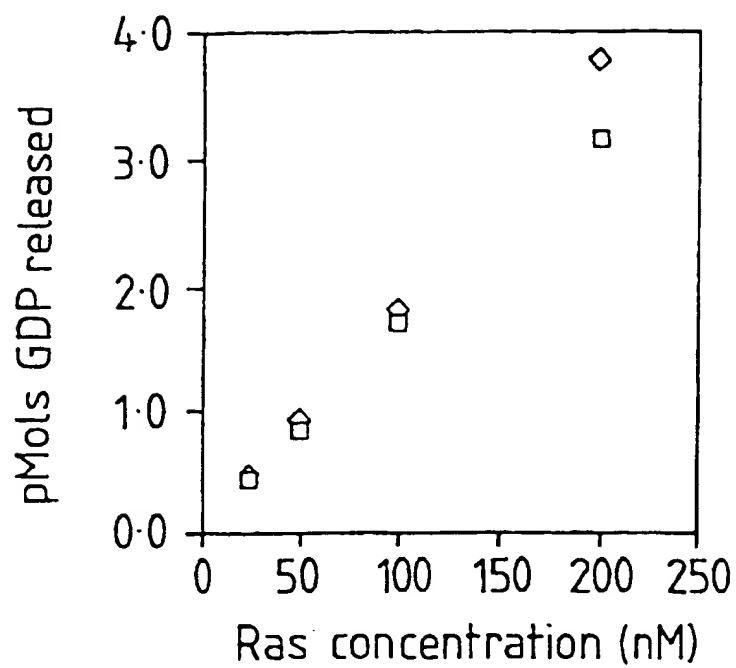
CTC CAG ATA GCC	ACG ATT	TCA TTC	CTC CTC	GCT CCC	CAC CAC	AGG AGG	TCC TCC	350
Leu Gln Ile Ala	Thr Ile	Ser Phe	Leu Leu	Ala Ala	Pro His	Arg Arg	Ser Ser	
75	80	85						
CTC TCC CCA AAA	TAT TCC	CAT CTT	GTC GTC	CTA GCC	CAT CAT	CCC CCC	CCA CCA	392
Leu Ser Pro Lys	Tyr Ser	His Leu	Val Val	Leu Leu	Ala His	Pro Pro	Pro Pro	
90	95	100						
GAC TAT CTC AAG	GAC CAG	CTG CTG	TCC CCA	CGC CGC	CGA CGA	CCT CCT	CCA CCA	434
Asp Tyr Leu Lys	Asp Gln	Leu Leu	Pro Ser	Arg Pro	Arg Pro	Pro Pro	Pro Pro	
105	110	115						
CTA GGC CTG TGC	CAC CCG	CTG CCT	GCA GCA	GGA GGA	AGA CGC	CCG CCG	GTC GTC	476
Leu Gly Leu Cys	His Pro	Leu Leu	Ala Ala	Gly Gly	Arg Arg	Pro Pro	Val Val	
120	125	130						
CCG GGC CGG GTT	AGC AGC	ATG GGA	ACG ACG	CAG CAG	CGC CTG	TGT TGT	GGC GGC	518
Pro Gly Arg Val	Ser Ser	Met Met	Gly Gly	Gln Thr	Arg Arg	Leu Leu	Cys Cys	
130	135	140						

54/85

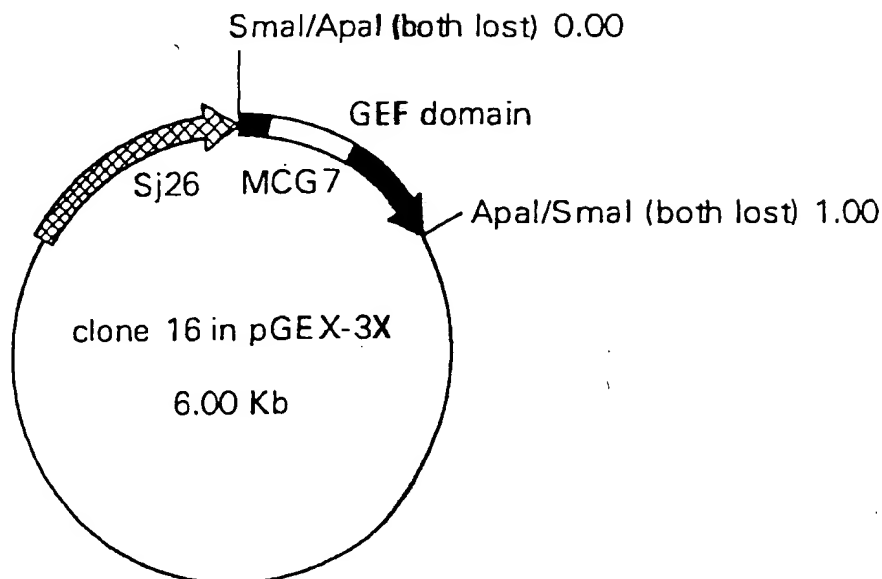
FIGURE 16 (III)

CGC GGG ACT CAA	GGC TGG CCT GGC TCA AGT GAA CAG CAC GTC	560
Arg Gly Thr Gln 145	Pro Gly Trp 150	
	Gln Ala Thr 155	
CAG GAG GCG ACC TCG TCC TCG GGT TTG CAT TCT GGG GTG GAC		602
Gln Glu Ala Thr 155	Ala Gly Leu His Ser Gly Val Asp 165	
	Glu 160	
GAG CTG GGG GTT CGG TCC GAG CCC GGT GGG AGG CTC CCG GAG		644
Glu Leu Gly Val 170	Glu Pro Gly Arg Leu Pro Glu 180	
	Arg Ser 175	
CGC AGC CTG GGC CCA GCC CAC CCG GCG GCC ATG GCA		686
Arg Ser Leu Gly 185	Pro Ala Pro Ala Met Ala 190	
	Pro Arg 185	
GGC ACC CTG GAC CTG GAC AAG GGC TGC ACG GTG G		720
Gly Thr Leu Asp 195	Leu Asp Cys Thr Val 205	
	Asp 200	

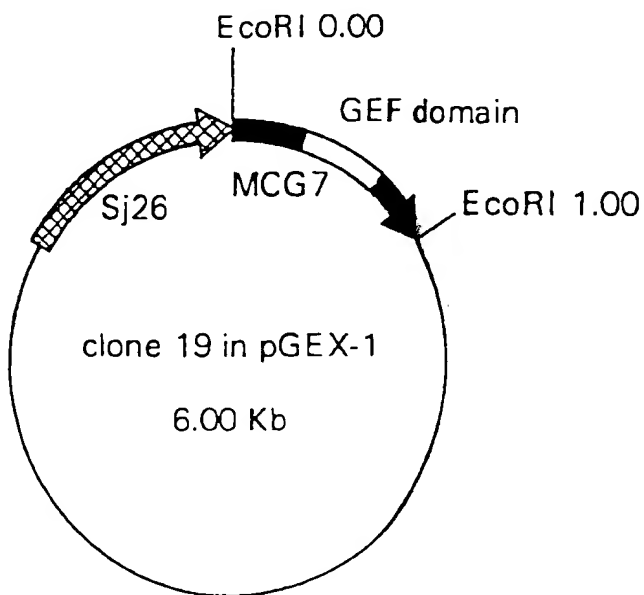
55/85

FIGURE 17

56/85

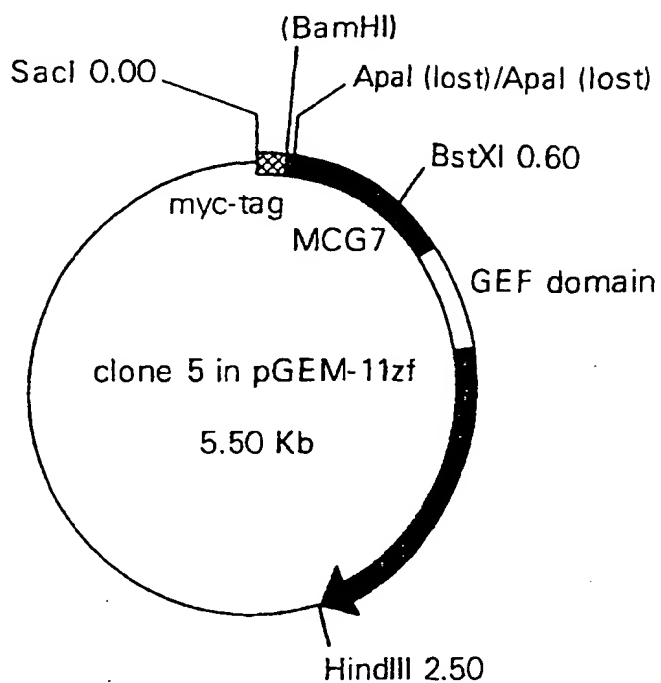
FIGURE 18 (Cont. I)

Plasmid name: clone 16 in pGEX-3X
Plasmid size: 6.00 kb

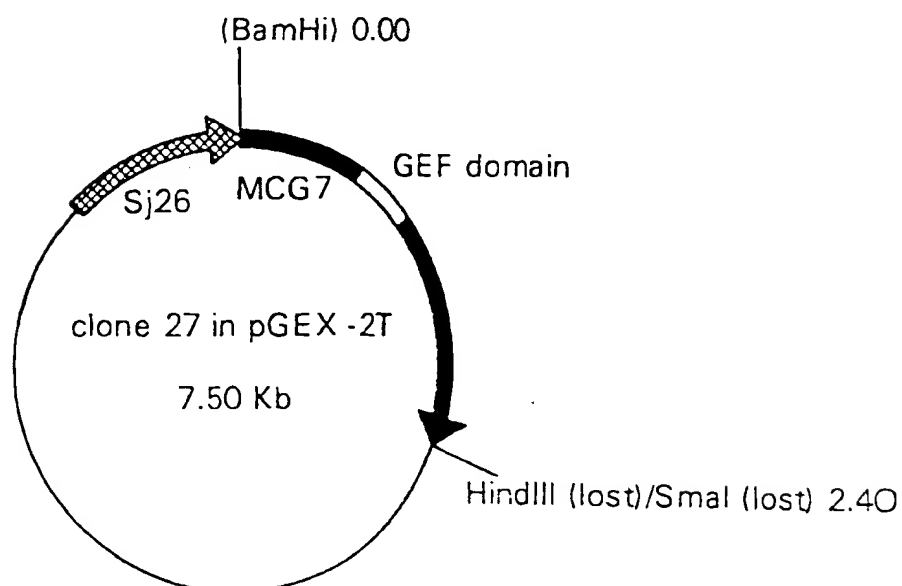
FIGURE 18 (Cont. II)

Plasmid name: clone 19 in pGEX-1
Plasmid size: 6.00 Kb

57/85

FIGURE 18 (Cont. III)

Plasmid name: clone 5 in pGEM-11zf
Plasmid size: 5.50 kb



Plasmid name: clone 27 in pGEX-2T
Plasmid size: 7.50 kb

FIGURE 18 (Cont. IV)

SUBSTITUTE SHEET (RULE 26)

58/85

FIG 19 (I)FIG 19 (II)FIG 19 (III)FIG 19 (IV)FIG 19

59/85

43
 85
 127
 169
 211
 253

FIGURE 19 (I)
 GCGCGCGCC ATG CCG CCC TTA CTG CCC CTG CGC CTG TGC CGG
 Met Pro Pro Leu Leu Leu Pro Leu Arg Leu Cys Arg
 1 5 10
 CTG TGG CCC AAC CCT CCC TCC CGG CTC CTC GGA GCG GCC
 Leu Trp Pro Arg Asn Pro Pro Ser Arg Leu Leu Gly Ala Ala
 15 20 25
 GCC GGG CAG CGG TCC AGA CCC AGT ACT TAT TAT GAA CTG TTG
 Ala Gly Gln Arg Ser Arg Pro Ser Thr Tyr Tyr Glu Leu Leu
 30 35
 GGG GTG CAT CCT GGT GCC AGC ACT GAG GAA GTT AAA CGA GCT
 Gly Val His Pro Gly Ala Ser Thr Glu Glu Val Lys Arg Ala
 40 45 50
 TTC TTC TCC AAG TCC AAA GAG CTG CAC CCA GAC CGG GAC CCT
 Phe Phe Ser Lys Ser Lys Glu Leu His Pro Asp Arg Asp Pro
 55 60 65
 GGG AAC CCA AGC CTG CAC AGC CGC TTT GTG GAG CTG AGC GAG
 Gly Asn Pro Ser Leu Leu His Ser Arg Phe Val Glu Leu Ser Glu
 70 75 80

1. The first step is to identify the problem or question that needs to be addressed. This involves understanding the context and the specific requirements of the task.

GCA Ala	TAC Tyr	CGT Arg	GTG Val	CTC Leu	AGC Ser	GAG Glu	CAG Gln	AGC Ser	CGC Arg	CGC Arg	AGC Ser	TAT Tyr	295
85													
GAT Asp	GAC Asp	CAG Gln	CTC Leu	CGC Arg	TCA Ser	GGT Gly	AGT Ser	CCC Pro	CCA Pro	AAG Lys	TCT Ser	CGA Arg	337
100													
ACC Thr	ACA Thr	GTC Val	CAT His	GAC Asp	AAG Lys	TCT Ser	GCC Ala	CAC His	CAA Gln	ACA Thr	CAC His	TCC Ser	379
115													
TGG Trp	ACA Thr	CCC Pro	CCC Pro	AAC Asn	GCA Ala	CAG Gln	TAC Tyr	TGG Trp	TCC Ser	CAG Gln	TTT Phe	AGC Ser	421
125													
GTG Val	AGG Arg	CCA Pro	CAG Gln	GGG Gly	CCC Pro	CAG Gln	TTG Leu	AGG Arg	CAG Gln	CAA Gln	CAC His	AAA Lys	463
140													
CAA Gln	AAC Asn	AAA Lys	CAA Gln	GTG Val	CTG Leu	GGG Gly	TAC Tyr	TGC Cys	CTC Leu	CTC Leu	ATG Met	CTG Leu	505
155													
160													
165													

61/85

FIGURE 19 (III)

GCG GGC ATG GGC CTG CAC TAC ATT GCC TTC AGG AAG GTG AAG		547
Ala Gly Met Gly Leu 170	His Tyr Ile Ala Phe Arg Lys Val Lys	
CAG ATG CAC CTT AAC TTC ATG GAT GAA AAG GAT CGG ATC ATC		589
Gln Met His Leu Asn 185	Phe Met Asp Glu Lys Asp Arg Ile Ile	
ACA GCC TTC TAC TAC AAC GAA GCC CGG GCA CGG GCC AGG GCC AAC		631
Thr Ala Phe Tyr Asn 195	Glu Gln Ala Arg Ala Arg Ala Asn	
AGA GGC ATC CTT CAG CAG GAG CGA CAA CGG CTA GGG CAG CGG		673
Arg Gly Ile Leu 210	Gln Gln Gln Arg Gln Leu Gly Gln Arg	
CAG CCG CCA CCA TCC GAG CCA ACC CAA GGC CCC GAG ATC GTG		715
Gln Pro Pro Pro Ser 225	Glu Glu Pro Thr Gln Gln Pro Glu Ile Val	
CCC CGG GGC GCC GGC CCC TGA GGGGCTC ACCTGGATGG GGCCTGCAGT		763
Pro Arg Gly Ala Gly 240	Pro * Pro	

62/85

FIGURE 19 (IV)

GCGTTCCCGC TTTGCTTCCT TCCCTGGACG GCCCGCTCCC CGAAACGCGC

813

GCAATAAAGT GATTCGCAG

832

FIGURE 20

>sp|P08622|DNAJ_ECOLI DNAJ PROTEIN >pir ||HHECDJ heat shock protein
dnaJ -

Escherichia coli >gi |145769 (M12565)-heat shock protein dnaJ

[Escherichia coli] >gi |216441 (D10483) dnaJ protein

[Escherichia coli]

Length = 376

Score = 138 (63.7 bits), Expect = 1.2e-10, P = 1.2e-10

Identities = 25/62 (40%), Positives = 39/62 (62%)

63/85

Query: 35 YYELGVHPGASTE EVKRAFFSKSKELHPDRDPGNPSLHSR FVELSEAYRVLSREQSRRS94

YYE+LGV A E+++A+ + + HPDR+ G+ ++F E+ EAY VL+ Q R +

Sbjct: 6 YYEILGVSKTAEEREIRKAYKRLAMKYHPDRNQGDKEAEAKFKEIKEYEVLTD SQKRAA65

Query: 95 YD 96

YD

Sbjct: 66 YD 67

64/85

FIG 21 (I)

FIG 21 (II)

FIG 21 (III)

FIG 21 (IV)

FIG 21

65/85

FIGURE 21 (I)

>gi|1703590 (U80439) contains similarity to a DNAJ-like domain
 (Caenorhabditis elegans)

Length = 345

Score = 98 (45.2 bits), Expect = 5.2e-12, Sum P(3) = 5.2e-12
 Identities = 17/37 (45%), Positives = 28/37 (75%)

Query: 28 QRSRPSTYYELLGVHPGASTEVEVKRAFFSKSKELHPD 64
 ++ R T+YE+LGV A+ E+K AF+++SK++HPD

Sbjct: 22 KKIRQTHYEVLGVESTATLSEIKSAFYAQSKKVHPD 58

Score = 74 (34.1 bits), Expect: = 5.2e-12, Sum P(3) = 5.2e-12
 Identities = 17/32 (53%), Positives = 19/32 (59%)

66/85

FIGURE 21 (II)

Query: 71 SLHSRFVELSEAYRVLRSREQRRSYDDQLRSG 102

S + F+EL AY VL R RR YD QLR G

Sbjct: 64 SATASFLELKNAYDVLRRPADRRRLYDYQLRGG 95

Score = 39 (18.0 bits), Expect = 5.2e-12, Sum P(3) = 5.2e-12
Identities = 10/42 (23%), Positives = 19/42 (45%)

Query: 162 LMLAGMGLHYIAFRKVKQMHLNFMDEKDRIITAFYNEARAR 203

L+++AG Y+ Q L+ + ++D I F + R

Sbjct: 158 LVLVAGYNGGYLLAYNQQLDKLIDEDIEIAKCFLRQKEFR 199

added" attached

WO 98/53061

CT/AU98/00380

09/424458

67/85

FIGURE 21 (III)
>gnl |PID |e281266 (Z81030) COLG10.12 [Caenorhabditis elegans]

Length = 191
Score = 96 (44.3 bits), Expect = 1.8e-09, Sum P(3) = 1.8e-09
Identities = 17/41 (41%), Positives = 27/41 (65%)

Query: 35 YYELGVHPGASTEVEVKRAFFSKSKELHPDRDPCNP SLHSR 75
YYE++GV A+ +E++ AF K+K+LHPD+ + SR
Sbjct: 19 YYEIIIGVSASATRQEIRDAFLKKTQLHPDQSRKSSKSDSR 59

Score = 54 (24.9 bits), Expect = 1.8e-09, Sum P(3) = 1.8e-09
Identities = 10/22 (45%), Positives = 15/22 (68%)

Query: 75 RFVELSEAYRVLSREQSRRSYD 96
+F+ + EAY VL E+ R+ YD

68/85

FIGURE 21 (IV)

Sbjct: 71 QFMLVKEAYDVLNRNEEKREYD 92

Score = 35 (16.1 bits), Expect = 1.8e-09, Sum P(3) = 1.8e-09
 Identities = 9/44 (20%), Positives = 22/44 (50%)

Query: 141 QGPQLRQQQHKQNKQVLGYCLLLMLAGMGLHYIAFRKVKQMHLN 184
 + P+ + KQ ++L ++A +G + + RK++ L+
 Sbjct: 145 RNPDEYLRKQKQNRMLVVLAATVMALIGANIVYIRKLQADRLS 188

69/85

FIG 22 (I)

FIG 22 (II)

FIG 22 (III)

FIG 22

70/85

FIGURE 22 (I)

>sp|Q10209|YAY1_SCHPO HYPOTHETICAL 44.8 KD PROTEIN C4H3.01 IN
CHROMOSOME I
>gi|1184014 (Z69380) unknown [Schizosaccharomyces pombe]
Length = 392

Score = 84 (38.8 bits), Expect = 4.1e-08, Sum P(3) = 4.1e-08
Identities = 13/36 (36%), Positives = 25,36 (69%)

Query: 35 YYELLGVHPGASTEVEVKRAFFSKSKELHPDRDPGNP 70

YY+LLG+ A+ ++K+A+ + + HPD++P +P

Sbjct: 9 YYDLLGISTDATAVDIKKAYRKLAVKYHPDKNPDDP 44

Score = 64 (29.5 bits), Expect = 4.1e-08, Sum P(3) = 4.1e-08
Identities = 14/40 (35%), Positives = 23/40 (57%)

12345678910111213141516171819202122232425262728293031323334353637383940414243444546474849505152535455565758596061626364656667686970717273747576777879808182838485868788899091929394959697989910010110210310410510610710810911011111211311411511611711811912012112212312412512612712812913013113213313413513613713813914014114214314414514614714814915015115215315415515615715815916016116216316416516616716816917017117217317417517617717817918018118218318418518618718818919019119219319419519619719819920020120220320420520620720820921021121221321421521621721821922022122222322422522622722822923023123223323423523623723823924024124224324424524624724824925025125225325425525625725825926026126226326426526626726826927027127227327427527627727827928028128228328428528628728828929029129229329429529629729829930030130230330430530630730830931031131231331431531631731831932032132232332432532632732832933033133233333433533633733833934034134234334434534634734834935035135235335435535635735835936036136236336436536636736836937037137237337437537637737837938038138238338438538638738838939039139239339439539639739839940040140240340440540640740840941041141241341441541641741841942042142242342442542642742842943043143243343443543643743843944044144244344444544644744844945045145245345445545645745845946046146246346446546646746846947047147247347447547647747847948048148248348448548648748848949049149249349449549649749849950050150250350450550650750850951051151251351451551651751851952052152252352452552652752852953053153253353453553653753853954054154254354454554654754854955055155255355455555655755855956056156256356456556656756856957057157257357457557657757857958058158258358458558658758858959059159259359459559659759859960060160260360460560660760860961061161261361461561661761861962062162262362462562662762862963063163263363463563663763863964064164264364464564664764864965065165265365465565665765865966066166266366466566666766866967067167267367467567667767867968068168268368468568668768868969069169269369469569669769869970070170270370470570670770870971071171271371471571671771871972072172272372472572672772872973073173273373473573673773873974074174274374474574674774874975075175275375475575675775875976076176276376476576676776876977077177277377477577677777877978078178278378478578678778878979079179279379479579679779879980080180280380480580680780880981081181281381481581681781881982082182282382482582682782882983083183283383483583683783883984084184284384484584684784884985085185285385485585685785885986086186286386486586686786886987087187287387487587687787887988088188288388488588688788888989089189289389489589689789889990090190290390490590690790890991091191291391491591691791891992092192292392492592692792892993093193293393493593693793893994094194294394494594694794894995095195295395495595695795895996096196296396496596696796896997097197297397497597697797897998098198298398498598698798898999099199299399499599699799899910001001100210031004100510061007100810091010101110121013101410151016101710181019102010211022102310241025102610271028102910301031103210331034103510361037103810391040104110421043104410451046104710481049105010511052105310541055105610571058105910601061106210631064106510661067106810691070107110721073107410751076107710781079108010811082108310841085108610871088108910901091109210931094109510961097109810991100110111021103110411051106110711081109111011111112111311141115111611171118111911201121112211231124112511261127112811291130113111321133113411351136113711381139114011411142114311441145114611471148114911501151115211531154115511561157115811591160116111621163116411651166116711681169117011711172117311741175117611771178117911801181118211831184118511861187118811891190119111921193119411951196119711981199120012011202120312041205120612071208120912101211121212131214121512161217121812191220122112221223122412251226122712281229123012311232123312341235123612371238123912401241124212431244124512461247124812491250125112521253125412551256125712581259126012611262126312641265126612671268126912701271127212731274127512761277127812791280128112821283128412851286128712881289129012911292129312941295129612971298129913

Query: 75 RFVELSEAYRVLSREQRRSYDDQLRSGSPKSPRTTVHD 114
+F ++SEAY+VL E+ R YD + + P+ T +D
Sbjct: 50 KFQKISEAYQVLGDEKLRSQYDQFGKEKAVPEQGTTDAYD 89

Score = 37 (17.1 bits), Expect = 4.1e-08, Sum P(3) = 4.1e-08
Identities = 9/29 (31%), Positives = 15/29 (51%)

Query: 190 DRIITAFYNEARARARANRGILQQERQRL 218
DR A E A A+ + +++ RQR+

Subjct: 149 DRKKNAQIREREALAKREQEMIEDRRQRI 177

Score = 33 (15.2 bits), Expect = 0.00081, Sum P(3) = 0.00081

Identities = 8/19 (42%), Positives = 11/19 (57%)

The first two columns of the table show the number of
 observations and the number of observations with non-missing
 values for each variable. The third column shows the
 variable name. The fourth column shows the variable
 type. The fifth column shows the variable label. The
 sixth column shows the variable format. The seventh
 column shows the variable range. The eighth column
 shows the variable mean. The ninth column shows the
 variable standard deviation. The tenth column shows the
 variable minimum. The eleventh column shows the
 variable maximum. The twelfth column shows the
 variable skewness. The thirteenth column shows the
 variable kurtosis. The fourteenth column shows the
 variable Jarque-Bera test statistic. The fifteenth
 column shows the variable Jarque-Bera test p-value.

Query: 140 P̄QGP̄QLR̄Q̄Q̄HK̄Q̄NK̄Q̄VLG 158
P̄Q̄G + Q̄+ + Q̄VLG
Sbjct: 44 P̄Q̄GASEKF̄Q̄K̄ĪSEAȲQ̄VLG 62

FIGURE 23

0.7e-13. p = 9.7e-13

Score = 153 (70.6 bits), Expect = 5.0e-32
Identities = 27/71 (38%), Positives = 44/71 (61%)

Query: 26

AGQSRSPSTYYELGGV... + R + YY LGV A+ +++K+A++ +K+ HPD + +F
 Subjct: 72 ... CUAKNANAKDIKKAYYELAKKYHPDTNKDDPDASKKFQDVSEAYEV 131

SSSRMQAQDYYATLGVA
Query: 86 LSREQRRSYD 96
LS +Q RR YD
Sbjct:132 LSDDQKRREYD 142

09/424458

CT/AU98/00380

WO 98/53061

74/85

FIG 24 (I)

FIG 24 (II)

FIG 24 (III)

FIG 24

Substitute Sheet (Rule 26)

75/85

FIGURE 24 (I)

MCG18 -----MPPLLPLRLCRLWP-RN--PP-----SRLLGAA
 HDJ-2 MVKETTYDVLGVKPNATQEELKKAYRKLALKYHPDKN--PN-----EGEKFKQISQAYEV
 HDJ-1 MGKD--YYQTLGLARGASDEEIKRAYRRQALRYHPDKNKEPG-----AEEKFKEIAEAYDV
 HSJ1 M-AS--YYEILDVPRASADDIKKAYRRKALQWHPDKN--PDNKEFAEKKFKEVAEAYEV
 * . * *
 AGQSRPSTY--YELLGVH-----PGA-----ST-EEVKRAFFS-
 LSDAKKRELYDKGGEQAIK-----EGGAGGG-----FGSPMDIFDMFFGGG
 LSDPRKREIFDRYGEGLKGGP-----SGSGGGANGTSFSYTFHGDPHAMFAEFFG--
 LSDKHKREIYDRYGREGLTGTGTPSRAEAGSGP--G--FTFT-FRSPPEVFRFFG-- **
 *
 KSKELHPDRDPGNP-----SLHSRFVELSEAYRVLREQRRS--YDDQLRSGSPPKSPRT
 GRMQRERRGKNVVHQLSVTLEDLYNGATRKLALQKNVICDKCEGRGGKKGAVECCPNCRG
 GRNPFDTFFGQRNGEEMDIDDPFSGFPMGMGGFTNVNFGRS--RSAQEPARKKQDPPVT
 SGDPFAELFDDLGP--FSELQNRGRSHSGPFFTFSSSPGHSDFSSSSFSPGAGAFRS
 ..

76/85

FIGURE 24 (II)

MCG18	TVHDKSAHQTHSSWTPNAQY-----WSQFHSVRPQ-----GP-----QLRQQQHKQN
HDJ-2	TGMQIRIHQIGPGMVQIQSVCMQCQGHGERISPK-DRCKSCNGRKIVREKKILEVHIDK
HDJ-1	HDLRVSLLEEIYSGCTKKMK-----ISH-KRLNP---D-----GKSIRNEDKILTIEVKK
HSJ-1	VSTSTTFVQGRRI TTRRIME-----NGQ-ERVEVEED-----GQ-----LKSVTINGVPD * . *
MCG18	KQVLGYCLLL-----MLAGMGLHYIAFRKVKQMHLNFMDE-KDRIITAFYNEARARAN
HDJ-2	GMKDGQKITFHGEGDQEPGLEPGDIIIVLDQKDHAVFTRRGEDLFMCMDIQLVEALCGFQ
HDJ-1	GWKEGTKITFPKEGDQTSNNIPADIVFVLKDKPHNIFKRDGSDVIYPARISLREALCGCT
HSJ1	DLARGLELSR-RE--QQP-SVTSRSGGTQVQQTTPASCPLD-SDLSEDEDLQAMAYSLSE * . *
MCG18	RGILQQERQRLGQRQPP-PSEPTQGPEIVPRGAGP-----
HDJ-2	KPISTLDNRTI VITSHPGQIVKHGDIKCVLNEGMPYRRPYEKGRLLIEFKVNFENGFL
HDJ-1	VNVPTLDGRTIPVVFK--DVIRPGMRKRKVPGEGLPLKTPKEKRGDLIIIEFEVIFPER--I
HSJ1	MEAAGKKPAGGREAQHR-RQGRPRPSTKIQAWGGP--RR--VRG--VKQPNVHPQR-RR * . *

77/85

FIGURE 24 (III)

MCG18	-----
HDJ-2	SPDKLSLLEKLLPERKEVEETDEMDQVELVDFDPNQERRRRHYNGEAYEDDEHHPRGGVQC
HDJ-1	PQTSRTVLEQVLPI
HSJ1	PLAASSSEHRAQPD-----LIQILTGGSDSLWEEKRGVS-----

MCG18	---
HDJ-2	QTS
HDJ-1	---
HSJ1	---

* = amino acid identity in all 4 proteins
- = conservative substitution

78/85

FIG 25 (I)

FIG 25 (II)

FIG 25(III)

FIG 25 (IV)

FIG 25

WO 98/53061

79/85

"GATE" attached

47
 89
 131
 173
 215
 257

FIGURE 25 (I)
 CAAGGAGCCT CTGCCCTGCCG GTCGTCGTC ATG CCG TCC CTG TTG CTC
 Met Pro Ser Leu Leu 5
 1
 CAG CTG CCC CTG CGC CTA TGC CCG CTG TGG CCG CAT AGC CTT
 Gln Leu Pro Leu Arg Leu Cys Arg Leu Trp Pro His Ser Leu 20
 10
 TCC ATC CGA CTT CTC ACA GCC GCC ACA GGG CAG CCG TCT GTC
 Ser Ile Arg Leu Leu Thr Ala Ala Thr Gly Gln Arg Ser Val 30
 25
 CCT ACT AAT TAC TAT GAA TTG TGG GGC GTG CAT CCG GGT GCC
 Pro Thr Asn Tyr Tyr Glu Leu Leu Gly Val His Pro Gly Ala 45
 40
 35
 AGC GCT GAA GAG ATT AAA CGT GCT TTT TTC ACC AAG TCA AAA
 Ser Ala Glu Glu Ile Lys Arg Ala Phe Phe Thr Lys Ser Lys 60
 55
 50
 GAG CTA CAC CCT GAT CGA GAC CCT GGG AAC CCA GCC CTG CAT
 Glu Leu His Pro Asp Arg Asp Pro Gly Asn Pro Ala Leu His 75
 65
 70

80/85

FIGURE 25 (II)

AGC	CGC	TTT	GTG	GAG	CTG	AAT	GAG	GCA	TAT	CGA	GTG	CTC	AGT	299
Ser	Arg	Phe	Val	Glu	Leu	Asn	Glu	Ala	Tyr	Arg	Val	Leu	Ser	
		80						85					90	
CGT	GAG	GAA	AGT	CGT	CGT	AAC	TAT	GAC	CAC	CAG	CTG	CAT	TCA	341
Arg	Glu	Glu	Ser	Arg	Arg	Asn	Tyr	Asp	His	Gln	Leu	His	Ser	
				95					100					
GCC	AGT	CCT	CCA	AAG	TCT	TCA	GGG	AGC	ACA	GCC	GAG	CCT	AAG	383
Ala	Ser	Pro	Pro	Lys	Ser	Ser	Gly	Ser	Thr	Ala	Glu	Pro	Lys	
105					110					115				
TAT	ACG	CAA	CAG	ACA	CAC	AGC	AGC	TCC	TGG	GAA	CCC	CCC	AAC	425
Tyr	Thr	Gln	Gln	Thr	His	Ser	Ser	Ser	Trp	Glu	Pro	Pro	Asn	
	120					125					130			
GGT	CAA	TAC	TGG	GCC	CAG	TTC	CAC	AGT	GTG	AGG	CCG	CAG	GGG	467
Ala	Gln	Tyr	Trp	Ala	Gln	Phe	His	Ser	Val	Arg	Pro	Gln	Gly	
		135					140					145		
CCG	GAG	TCA	AGG	AAG	CAG	CAG	CGT	AAA	CAC	AAC	CAG	CGG	GTC	509
Pro	Glu	Ser	Arg	Lys	Gln	Gln	Arg	Lys	His	Asn	Gln	Arg	Val	
			150					155					160	

WO 98/53061

81/85

COPIED "05442460"

551

593

635

677

719

FIGURE 25 (III)

CTG GGG TAC TGC CTC CTG CTC ATG GTG GCA GGC ATG GGC CTG
 Leu Gly Tyr Cys 165 Leu Leu Met Val 170
 CAC TAT GTT GCC TTC AGG AAG CTG GAG CAG GTG CAT CGC AGC
 His Tyr Val Ala Phe 180
 TTC ATG GAT GAA AAG GAC CGG ATC ATT ACA GCC ATC TAC AAT
 Phe Met Asp Glu Lys Asp 195
 GAC ACT CGG GCC AGG GCC AGG GCC AAC AGA GCC AGG ATT CAG
 Asp Thr Arg Ala Arg Ala Arg Ala Asn Arg Ala Arg Ile Gln
 205
 CAG GAG CGC CAC GAG AGG CAG CCT CGG GCA GAA CCC TCC
 Gln Glu Arg His Glu Arg Gln Gln Pro Arg Ala Glu Pro Ser
 220 230

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WO 98/53061

82/85

09 / 4 2 4 4 5 8

PCT/AU98/00380

761
814
849

FIGURE 25 (IV)

CTG CCT CCA GAA AGC TCC AGG ATC ATG CCC CAG GAC ACA AGC
Leu Pro Pro Glu Ser Ile Met Pro Gln Asp Thr Ser
235 240

CCC TGAGAGGCTT AACTAAATGG GACCTTCATT GGTCCTCTCC CTGCTGCCCTG
Pro
245

TCCAGAACTA CACGTGCAAT AAACCTCATT TCAG (A)n

83/85

CONFIDENTIAL

FIGURE 26

human	MCG18	MPPLL---PLRLCRLWPNPPSRLLGAAAGQSRSPSTYYELLGVHPGASAEIKRAFFTK
mouse	MCG18	MPSLLLQLPLRLCRLWPHSLSIRLLTAATGQRSVPTNYEYELLGVHPGASAEIKRAFFSK

```

human MCG18 MPFLLQPLRLCRLWPHSLSRLLIARCGT*****
mouse MCG18 MPFLLQPLRLCRLWPHSLSRLLIARCGT*****

```

```

**
**
human MCG18 SKELHPDRDPGNPSLHRSFVELSEAYRVLREQRRSYDDQLRSGSPPKSPRTTVHDKSA
mouse MCG18 SKELHPDRDPGNPALHRSFVELNEAYRVLREESRRNYDQLHSAFPKSSGSAEPKYT
**

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human MCG18 HQTHSS-WTPPNAQYWSQFHSVRPQGPQLRQQQHKQNKQVLGYCLLLMLAGMGLHYVAFR
mouse MCG18 QQTHSSWEPPNAQYWAQFHSVRPQGPESRKQQRKHNQRVLGYCLLLMVAGMGLHYVAFR

human MCG18 HQTHSS-WTPPNAQVWSE
mouse MCG18 QQTHSSWEPPNAQYWAQFHSVFPQGPESRKQQRKHNQKRVLDGIC

human MCG18 KVKQMHLNFMDEKDRIITAFYNEARARANRGILQQRQRLGQRQPPSEPTQGPE---
mouse MCG18 KLEQVHRSMDEKDRIITAIYNDTRARANRARIQQR---HERQQPRAEPSLPPESSR

human	MCG18	IVPRGAGP
mouse	MCG18	IMPQDTSP

84/85

FIGURE 27

TTGA AGT CTA GCC CCA TCC TGG TCC AAT GCG CTC TTG GTA	40
* Ser Leu Ala Pro Ser Trp Ser Asn Ala Leu Leu Val	
GCC TCC TTT CCC AGC TGC CCG CCC GCC ATG CCG CCC TTA	82
Ala Ser Phe Pro Ser Cys Pro Pro Ala Ala Met Pro Pro Leu	
CTG CCC CTG CGC CTG TGC CCG CTG TGG CCC CGC AAC CC	120
Leu Pro Leu Arg Leu Cys Arg Arg Leu Trp Pro Arg Asn Pro	

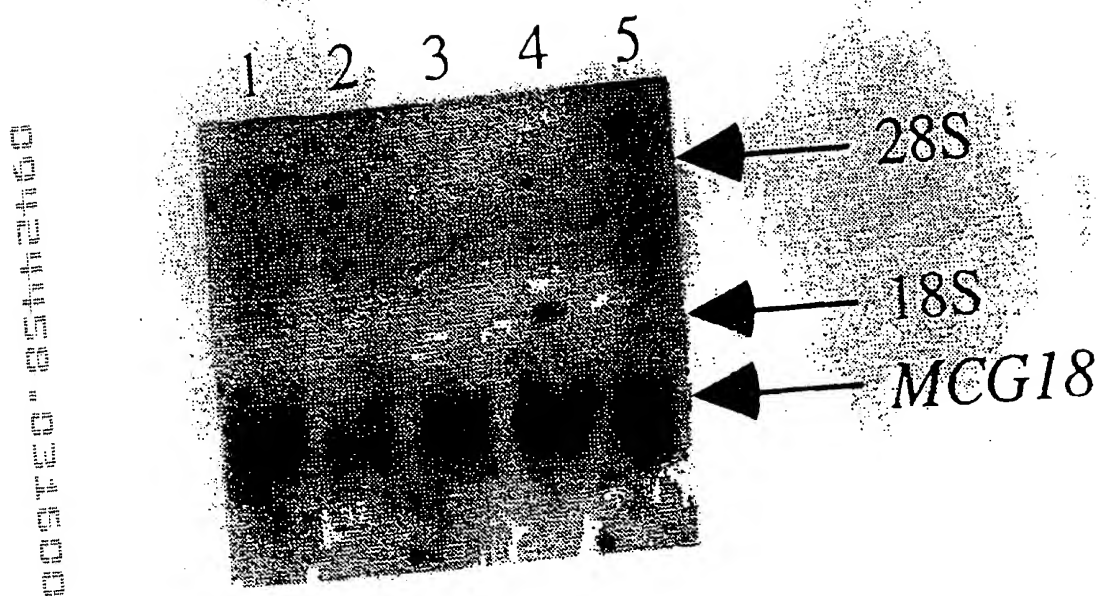


FIG 28